SEQUENCE LISTING

<110> Penttila, Merja E.
Ward, Michael
Wang, Huaming
Valkonen, Mari J.
Saloheimo, Markku

<120> Increased Production of Secreted
Proteins by Recombinant Eukaryotic Cells

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<141> 2001-03-23

<150> US 09/534,692
<151> 2000-03-24

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<213> Trichoderma reesei

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Thr Glu Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn
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Gln Lys Thr Asn Leu Ile Leu Val Glu Glu Leu Asn Arg Phe Arg Arg
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Val His Gln Asp Asp Gly Pro Phe Ser Ile Gly His Ser Phe Gly Leu
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Ser Ala Ala Leu Asp Ala Asp Arg Tyr Leu Leu Glu Ser Gln Leu Leu
            340                 345                 350
Ala Ser Pro Asn Ala Ser Thr Val Asp Asp Asp Tyr Leu Ala Gly Asp
        355                 360                 365
Ser Ala Ala Cys Phe Thr Asn Pro Leu Pro Ser Asp Tyr Asp Phe Asp
    370                 375                 380
Ile Asn Asp Phe Leu Thr Asp Asp Ala Asn His Ala Ala Tyr Asp Ile
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Ile His Asp Pro Glu Asn Gln Ile Pro Ser Arg His Ser Ile Gln Gln
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<212> DNA
<213> Aspergillus nidulans

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<213> Aspergillus nidulans

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Lys Pro Glu Glu Lys Lys Pro Ala Lys Lys Arg Lys Ser Trp Gly Gln
    50   55   60
Glu Leu Pro Val Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
65   70   75   80
Thr Glu Asp Glu Lys Glu Gln Arg Arg Ile Glu Arg Val Leu Arg Asn
                85   90   95
Arg Ala Ala Ala Gln Thr Ser Arg Glu Arg Lys Arg Leu Glu Met Glu
            100   105   110
Lys Leu Glu Ser Glu Lys Ile Asp Met Glu Gln Gln Asn Gln Phe Leu
        115   120   125
Leu Gln Arg Leu Ala Gln Met Glu Ala Glu Asn Asn Arg Leu Ser Gln
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Gln Val Ala Gln Leu Ser Ala Glu Val Arg Gly Ser Arg His Ser Thr
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Pro Thr Ser Ser Ser Pro Ala Ser Val Ser Pro Thr Leu Thr Pro Thr
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Leu Phe Lys Gln Glu Gly Asp Glu Val Pro Leu Asp Arg Ile Pro Phe
            180   185   190
Pro Thr Pro Ser Val Thr Asp Tyr Ser Pro Thr Leu Lys Pro Ser Ser
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    210   215   220
Gly Leu Glu Gly Asp Glu Ser Ala Leu Thr Leu Phe Asp Leu Gly Ala
225   230   235   240
Ser Ile Lys His Glu Pro Thr His Asp Leu Thr Ala Pro Leu Ser Asp
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Asp Asp Phe Arg Arg Leu Phe Asn Gly Asp Ser Ser Leu Glu Ser Asp
            260   265   270
Ser Ser Leu Leu Glu Asp Gly Phe Ala Phe Asp Val Leu Asp Ser Gly
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Pro Val Thr Leu Glu Asp Leu Glu Gln Thr Asn Gly Leu Ser Asp Ser
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<211> 451
<212> PRT
<213> Trichoderma reesei

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Asp Ser Val Ala Asp Ile Asp Ser Arg Leu Ser Val Ile Pro Glu Ser
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Gln Asp Ala Glu Asp Asp Glu Ser His Ser Thr Ser Ala Thr Ala Pro
65 70 75 80
Ser Thr Ser Glu Lys Lys Pro Val Lys Lys Arg Lys Ser Trp Gly Gln
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Val Leu Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
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Thr Glu Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn
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225 230 235 240
Pro Ile Ser Asp Lys Glu Phe Gln Thr Lys Glu Glu Asp Glu Glu Gln
245 250 255
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355 360 365
Ser Ala Ala Cys Phe Thr Asn Pro Leu Pro Ser Asp Tyr Asp Phe Asp
370 375 380
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385 390 395 400
Val Ala Ala Ser Asn Tyr Ala Ala Ala Asp Arg Glu Leu Asp Leu Glu
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<212> PRT
<213> Aspergillus nidulans

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Gln Val Ala Gln Leu Ser Ala Glu Val Arg Gly Ser Arg His Ser Thr
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180 185 190
Pro Thr Pro Ser Val Thr Asp Tyr Ser Pro Thr Leu Lys Pro Ser Ser
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Gly Leu Glu Gly Asp Glu Ser Ala Leu Thr Leu Phe Asp Leu Gly Ala
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Ser Ile Lys His Glu Pro Thr His Asp Leu Thr Ala Pro Leu Ser Asp
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Asp Asp Phe Arg Arg Leu Phe Asn Gly Asp Ser Ser Leu Glu Ser Asp
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Ser Ser Leu Leu Glu Asp Gly Phe Ala Phe Asp Val Leu Asp Ser Gly
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Asp Leu Ser Ala Phe Pro Phe Asp Ser Met Val Asp Phe Asp Thr Glu
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<212> DNA

<213> Aspergillus nidulans

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35 40 45
Ile Ala Ala Lys Gln Asp Leu Tyr Arg Ile Cys Glu Asn Met Met Asp
50 55 60
Asn Cys Leu Ala Ser Asn Ser Glu Thr Gly Gly Val Gly Cys Asp Asn
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<400> 9

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<400> 10

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            20                  25                  30
Arg Ile Ser Met Glu Asp Ala His Thr Ala Glu Leu Asn Leu Pro Pro
        35                  40                  45
Pro Asp Asn Asp Thr Lys Thr His Pro Asp Arg Leu Ser Phe Phe Gly
    50                  55                  60
Val Phe Asp Gly His Gly Gly Asp Lys Val Ala Leu Phe Ala Gly Glu
65                  70                  75                  80
Asn Ile His Asn Ile Val Phe Lys Gln Glu Ser Phe Lys Ser Gly Asp
                85                  90                  95
Tyr Ala Gln Gly Leu Lys Asp Gly Phe Leu Ala Thr Asp Arg Ala Ile
            100                 105                 110
Leu Asn Asp Pro Lys Tyr Glu Glu Glu Val Ser Gly Cys Thr Ala Cys
        115                 120                 125
Val Thr Leu Ile Ala Gly Asn Lys Leu Tyr Val Ala Asn Ala Gly Asp
    130                 135                 140
Ser Arg Ser Val Leu Gly Ile Lys Gly Arg Ala Lys Pro Leu Ser Asn
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145                 150                 155                 160
Asp His Lys Pro Gln Leu Glu Thr Glu Lys Asn Arg Ile Thr Ala Ala
                165                 170                 175
Gly Gly Phe Val Asp Phe Gly Arg Val Asn Gly Asn Leu Ala Leu Ser
            180                 185                 190
Arg Ala Ile Gly Asp Phe Glu Phe Lys Lys Ser Ala Glu Leu Ser Pro
        195                 200                 205
Glu Asn Gln Ile Val Thr Ala Phe Pro Asp Val Glu Val His Glu Leu
    210                 215                 220
Thr Glu Glu Asp Glu Phe Leu Val Ile Ala Cys Asp Gly Ile Trp Asp
225                 230                 235                 240
Cys Gln Ser Ser Gln Ala Val Val Glu Phe Val Arg Arg Gly Ile Ala
                245                 250                 255
Ala Lys Gln Asp Leu Asp Lys Ile Cys Glu Asn Met Met Asp Asn Cys
            260                 265                 270
Leu Ala Ser Asn Ser Glu Thr Gly Gly Val Gly Cys Asp Asn Met Thr
        275                 280                 285
Met Val Ile Ile Gly Phe Leu His Gly Lys Thr Lys Glu Glu Trp Tyr
    290                 295                 300
Asp Glu Ile Ala Lys Arg Val Ala Asn Gly Asp Gly Pro Cys Ala Pro
305                 310                 315                 320
Pro Glu Tyr Ala Glu Phe Arg Gly Pro Gly Val His His Asn Tyr Glu
                325                 330                 335
Asp Ser Asp Ser Gly Tyr Asp Val Asp Ala Asp Ser Gly Gly Lys Phe
            340                 345                 350
Ser Leu Ala Gly Ser Arg Gly Arg Ile Ile Phe Leu Gly Asp Gly Thr
        355                 360                 365
Glu Val Leu Thr Gly Ser Asp Asp Thr Glu Met Phe Asp Asn Ala Asp
    370                 375                 380
Glu Asp Lys Asp Leu Ala Ser Gln Val Pro Lys Ser Ser Gly Lys Thr
385                 390                 395                 400
Asp Ala Lys Glu Glu Thr Glu Ala Lys Pro Ala Pro Glu Ala Glu Ser
                405                 410                 415
Ser Lys Pro Ala Asp Gly Ser Glu Lys Lys Gln Asp Glu Lys Thr Pro
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Glu Glu Ser Lys Lys Asp
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<210> 11
<211> 1570
<212> DNA
<213> Aspergillus nidulans

<400> 11

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cactgcatct aatgaggtgt ttgaagcgga cggtgtcatc cagattggcc gtttgaaggt     180
ctttacggct gacgttctgg gtcatggaag ccacgggaca gttgtttacc gcgggtcgtt     240
tgacggccga gacgtcgcgg tcaaacgtat gctggtggag ttctatgata ttgcatcgca     300
cgaagtggga ttgttgcagg aaagcgatga tcataacaac gttatccgat gttattgccg     360
tgagcaagcc aagggtttct tctacatcgc ccttgaactg tgtccggctt ctttgcagga     420
tgtggtagaa cgaccagacg cgttcccgca gctagtcaat ggtggcttgg atatgccgga     480
cgtcttgcgt caaattgtcg ccggtgtccg gtacctacac tctctcaaaa tcgtacaccg     540
tgacttgaag cctcaaaata tcctggtcgc cgctcctcga ggccgtatcg gttctcgggc     600
catccggctt ctgatttcgg actttggctt gtgcaagaaa cttgaggata accagagttc     660
attcagggca accacggccc atgctgctgg tactccgggt ggagggctcc cgaactgctt     720
gtggatgacg acaagagccg gtaatcaggg ttcagagtct caaaatacgg agtcatctga     780
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gccggcggtc gtcgatcccc agacgaatcg acgagccacc cgagccattg atatcttctc     840
cctgggatgt gtcttctact acgtcctaac tcgaggatgt catccttttg acaagaatgg     900
caagttcatg cgcgaagcaa atatcgtcaa ggggaatttc aatctcgatg agttacagcg     960
tctaggagag tatgcgtttg aagcagacga tcttatccga tcaatgttgg cacttgatcc    1020
acgtcaacgg tatgtcccaa caacatcttc ctttgccttg tggcgtagcg tactaatctc    1080
cacagccccg acgcaagcgc tgtgttaacc catcctttct tctggaatcc gtccgaccgc    1140
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caaactcctg ccaaaggact tcaaagacag tctcggaagc agcgaaaata caccggctcc    1320
aaaatgctgg acttgatgcg agccctgcgg aacaagcgca accactacaa tgatatgccg    1380
gagcatttga aagctcatat tggtgggctg ccggagggtt acttgaattt ctggaccgtg    1440
cgtttcccga gtttgctgat gagttgtcat tgggtgattg ttgaactggg attgacgaag    1500
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<210> 12
<211> 504
<212> PRT
<213> Aspergillus nidulans

<400> 12

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Glu Glu Ser Asp His Ala Pro Gly Thr Leu Gln Pro Pro Ala Gly Pro
            20                  25                  30
Asp Ala Gly Leu Ala Leu Thr Arg Thr Ala Ser Asn Glu Val Phe Glu
        35                  40                  45
Ala Asp Gly Val Ile Gln Ile Gly Arg Leu Lys Val Phe Thr Ala Asp
    50                  55                  60
Val Leu Gly His Gly Ser His Gly Thr Val Val Tyr Arg Gly Ser Phe
65                  70                  75                  80
Asp Gly Arg Asp Val Ala Val Lys Arg Met Leu Val Glu Phe Tyr Asp
                85                  90                  95
Ile Ala Ser His Glu Val Gly Leu Leu Gln Glu Ser Asp Asp His Asn
            100                 105                 110
Asn Val Ile Arg Cys Tyr Cys Arg Glu Gln Ala Lys Gly Phe Phe Tyr
        115                 120                 125
Ile Ala Leu Glu Leu Cys Pro Ala Ser Leu Gln Asp Val Val Glu Arg
    130                 135                 140
Pro Asp Ala Phe Pro Gln Leu Val Asn Gly Gly Leu Asp Met Pro Asp
145                 150                 155                 160
Val Leu Arg Gln Ile Val Ala Gly Val Arg Tyr Leu His Ser Leu Lys
                165                 170                 175
Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu Val Ala Ala Pro
            180                 185                 190
Arg Gly Arg Ile Gly Ser Arg Ala Ile Arg Leu Leu Ile Ser Asp Phe
        195                 200                 205
Gly Leu Cys Lys Lys Leu Glu Asp Asn Gln Ser Ser Phe Arg Ala Thr
    210                 215                 220
Thr Ala His Ala Ala Gly Thr Pro Gly Gly Gly Leu Pro Asn Cys Leu
225                 230                 235                 240
Trp Met Thr Thr Arg Ala Gly Asn Gln Gly Ser Glu Ser Gln Asn Thr
                245                 250                 255
Glu Ser Ser Glu Pro Ala Val Val Asp Pro Gln Thr Asn Arg Arg Ala
            260                 265                 270
Thr Arg Ala Ile Asp Ile Phe Ser Leu Gly Cys Val Phe Tyr Tyr Val
        275                 280                 285
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Leu Thr Arg Gly Cys His Pro Phe Asp Lys Asn Gly Lys Phe Met Arg
    290                 295                 300
Glu Ala Asn Ile Val Lys Gly Asn Phe Asn Leu Asp Glu Leu Gln Arg
305                 310                 315                 320
Leu Gly Glu Tyr Ala Phe Glu Ala Asp Asp Leu Ile Arg Ser Met Leu
                325                 330                 335
Ala Leu Asp Pro Arg Gln Arg Pro Asp Ala Ser Ala Val Leu Thr His
            340                 345                 350
Pro Phe Phe Trp Asn Pro Ser Asp Arg Leu Ser Phe Leu Cys Asp Val
        355                 360                 365
Ser Asp His Phe Glu Phe Glu Pro Arg Asp Pro Pro Ser Asp Ala Leu
    370                 375                 380
Leu Cys Leu Glu Ser Val Ala Ser Asp Val Ile Gly Pro Glu Met Asn
385                 390                 395                 400
Pro Gln Thr Pro Ala Lys Gly Leu Gln Arg Gln Ser Arg Lys Gln Arg
                405                 410                 415
Lys Tyr Thr Gly Ser Lys Met Leu Asp Leu Met Arg Ala Leu Arg Asn
            420                 425                 430
Lys Arg Asn His Tyr Asn Asp Met Pro Glu His Leu Lys Ala His Ile
        435                 440                 445
Gly Gly Leu Pro Glu Gly Tyr Leu Asn Phe Trp Thr Val Arg Phe Pro
    450                 455                 460
Ser Leu Leu Met Ser Cys His Trp Val Ile Val Glu Leu Gly Leu Thr
465                 470                 475                 480
Lys Thr Asp Arg Phe Gln Glu Ile Phe Tyr Ala Ile Gly Val Gly Cys
                485                 490                 495
Cys Val Leu Val Gln Lys Tyr Ile
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<210> 13
<211> 4528
<212> DNA
<213> Trichoderma reesei

<400> 13

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agcccacgat cgaatccaca gcctgcacca ctttctcctc gtcatattcg cggggactca     180
caagcggttt ccgttgcctt cgaattcgac agagctgcga ctgcgagtca tttcagcgac     240
tctaaaccta ctcctttggc tgctgcgcgg gactggttct gcccagcctc tcctactcga     300
ccaaccgacg tcctctttct gcttcctcat ccctttctcc tttgacgtcc gagcgtcaga     360
gcgaattttt ccttgcttct tcgtttgggc cgggaatggc ttctctggca tcgcaacagc     420
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tctccggcac cccgactttc gtctcgatca tgatgcggcg acccccgagc caaggacgat     540
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acttgccgat gctcagcagc agcctcagca gccccagatt cgaattcact cacaaagagg     660
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tgcaccagac gtgcaccccg aagcgaagtt cgacaccgtc aacaggaagc aaaagcagca     780
gtcgaccgct tcgccccagc aacaccagaa atatcgacga gccccctatg actacgccag     840
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cgacgactat cgccccgtcg accactacat ctgggccgtc gagccgagcc gcgatggagg    1260
gctctatgta tggatccccg actccggagc gggcctcgtc aggaccggct tcaccatgaa    1320
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gcacctcgtt gaagaacttg ctccatacgc cggcgacgag ccccccgttg tctataccgg 1380
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<210> 14
<211> 1232

<212> PRT
<213> Trichoderma reesei

<400> 14
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Gln Ile Arg Ile His Ser Gln Arg Gly Asp Ala Pro Leu Asp Lys Val
35 40 45
Ala Asp Asp Ala Asn Thr Arg Trp Tyr Ala Thr His Ala Ala Pro Asp
50 55 60
Val His Pro Glu Ala Lys Phe Asp Thr Val Asn Arg Lys Gln Lys Gln
65 70 75 80
Gln Ser Thr Ala Ser Pro Gln Gln His Gln Lys Tyr Arg Arg Ala Pro
85 90 95
Tyr Asp Tyr Ala Ser Lys Asp Lys Ala Gln Asn Arg Tyr Ala Gln His
100 105 110
Pro Ile Arg Glu Ser Glu Lys Pro Asn Tyr Val Lys Val Pro Asn Asp
115 120 125
Ala Ser Ala Leu Ala Thr Leu Ala Pro Ala Gln Pro Val Arg Ala Pro
130 135 140
His Thr Ser Arg His His Trp Pro Ser Ser Ser Ala Ala Ser Gly Leu
145 150 155 160
Ala Ser Pro His Asn Ala Arg Ser Leu Glu Asp Trp Glu Val Glu Asp
165 170 175
Phe Val Leu Leu Ala Thr Val Asp Gly Asp Leu Tyr Ala Ser Asp Arg
180 185 190
Lys Thr Gly Arg His Leu Trp His Leu Glu Val Asp Gln Pro Val Val
195 200 205
Glu Thr Lys His Tyr Arg Thr Asn Asn Ser Val Leu Asp Asp Asp Tyr
210 215 220
Arg Pro Val Asp His Tyr Ile Trp Ala Val Glu Pro Ser Arg Asp Gly
225 230 235 240
Gly Leu Tyr Val Trp Ile Pro Asp Ser Gly Ala Gly Leu Val Arg Thr
245 250 255
Gly Phe Thr Met Lys His Leu Val Glu Glu Leu Ala Pro Tyr Ala Gly
260 265 270
Asp Glu Pro Pro Val Val Tyr Thr Gly Asp Lys Lys Thr Thr Met Val
275 280 285
Thr Leu Asp Ala Ala Thr Gly Arg Val Leu Lys Trp Phe Gly Ser Ser
290 295 300
Gly Ser Gln Val Asn Glu Ala Glu Ser Cys Leu Arg Pro Asn Ala Phe
305 310 315 320
Asp Asp Arg Asp Thr Thr Glu Cys Ser Ser Met Gly Thr Ile Thr Leu
325 330 335
Gly Arg Thr Glu Tyr Thr Val Gly Ile Gln Arg Arg Asp Gly Arg Pro
340 345 350
Ile Ala Thr Leu Lys Tyr Ala Glu Trp Gly Pro Asn Thr Phe Asp Ser
355 360 365
Asp Leu Tyr Gln Gln Tyr His Ala Ser Leu Asp Asn His Tyr Ile Thr
370 375 380
Ser Gln His Asp Gly Arg Ile Tyr Ala Phe Asp Lys Ser Gln Ala Glu
385 390 395 400
Asn Asp Leu Pro Leu Tyr Thr His Lys Phe Ser Ser Pro Val Ala Arg
405 410 415
Val Phe Asp Val Cys Arg Pro Trp Asp Ala Asn Ala Gly Ser Asn Pro

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            420                 425                 430
Glu Leu Val Val Leu Pro Gln Pro Pro Ile Pro Ala Leu Asp Glu Ser
        435                 440                 445
Thr Val Lys Met Arg Ser Asn Ser Ile Phe Leu Asn Gln Thr Glu Ser
    450                 455                 460
Gly Asp Trp Tyr Ala Leu Ser Gly Arg Ala Tyr Pro Leu Ile Leu Asp
465                 470                 475                 480
Ala Pro Val Ala Gln Ile Ser Arg Asp Asp Leu Trp Asp Met Ala His
                485                 490                 495
Ala Phe Asp Ser Ile Asn Pro Asn Lys Leu Ser Lys Ala Leu Val Gly
            500                 505                 510
Thr His Phe Leu Asn Pro Val Lys Ser Thr Gly Tyr His Gln Pro Pro
        515                 520                 525
Thr Leu Pro Ala Gly Ala Leu Asp Glu Tyr Tyr Glu Asp Leu Glu Asn
    530                 535                 540
Ala Ser Asn Asn Ala His Ala Val Thr Asn Thr Val Pro Glu Glu Pro
545                 550                 555                 560
Thr Ile Ile Thr Lys Val Lys Ala Leu Pro Gln Ser Ala Ala Asn Ser
                565                 570                 575
Val Ile Asp Phe Val Ser Asn Pro Ile Leu Ile Ile Phe Leu Ile Gly
            580                 585                 590
Ser Leu Ile Tyr Asn Glu Lys Lys Leu Arg Arg Ser Tyr His Arg Phe
        595                 600                 605
Arg Thr His Gly Thr Ile Lys Asp Val Tyr Pro Phe Phe Val Ile Glu
    610                 615                 620
Ser Glu Ala Gly Asp Glu Ser Gly Asp Asp Lys Asp Gly Val Phe Pro
625                 630                 635                 640
Ser Ser Pro Ser Pro Arg Ser Gln Pro Gln Asp Gln Asn Ala Glu Asp
                645                 650                 655
His Leu Ser Arg His Lys Val Glu Arg Asn Ala Gly Asp Gln Asp Lys
            660                 665                 670
Val Lys Asp Asn Arg Ser Leu His Asp Val Ser Asp Thr Leu Glu Pro
        675                 680                 685
Ser Asn Lys Thr Val Glu Lys Thr Ala Asp Val Val Lys Gln Val Asp
    690                 695                 700
Val Ala Gly Pro Asp Ala Pro Ser Thr Asp Ser Asn Gly Ala Ala Pro
705                 710                 715                 720
Glu Lys Lys Lys Lys Ala His Arg Gly Arg Arg Gly Gly Val Lys His
                725                 730                 735
Arg Lys Gly Arg Pro Thr Asp Gly Ser Gln Ser His Glu Asn Asp Pro
            740                 745                 750
Ala Leu Thr Thr Val Asp Glu Ala Val Ser Asn Ala Lys Lys Leu Gly
        755                 760                 765
Asp Arg Pro Ser Leu Glu Pro Asp Val Met Thr Ile Tyr Asn Asp Met
    770                 775                 780
Gln Ala Val Thr Gly Ser Val Ile Ser Met Gly Asn Ile Glu Val Asp
785                 790                 795                 800
Thr Asp Val Glu Leu Gly Met Gly Ser Asn Gly Thr Val Val Phe Ala
                805                 810                 815
Gly Arg Phe Asp Gly Arg Asp Val Ala Val Lys Arg Met Thr Ile Gln
            820                 825                 830
Phe Tyr Asp Ile Ala Thr Arg Glu Thr Lys Leu Leu Arg Glu Ser Asp
        835                 840                 845
Asp His Pro Asn Val Ile Arg Tyr Tyr Ser Gln Val Gln Arg Gly Asp
    850                 855                 860
Phe Leu Tyr Ile Ala Leu Glu Arg Cys Ala Ala Ser Leu Ala Asp Val
865                 870                 875                 880
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Ile Glu Lys Pro Tyr Ala Phe Gly Glu Leu Ala Lys Ala Gly Gln Lys
                885                 890                 895
Asp Leu Pro Gly Val Leu Tyr Gln Ile Thr Asn Gly Ile Ser His Leu
            900                 905                 910
His Ser Leu Arg Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu
        915                 920                 925
Val Asn Leu Asp Lys Asp Gly Arg Pro Arg Leu Leu Val Ser Asp Phe
    930                 935                 940
Gly Leu Cys Lys Lys Leu Glu Asp Arg Gln Ser Ser Phe Gly Ala Thr
945                 950                 955                 960
Thr Gly Arg Ala Ala Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu
                965                 970                 975
Leu Asp Asp Asp Gly Gln Asn Pro Ala Ala Ile Asp Ser Ser Thr His
            980                 985                 990
Ser Gly Ser His Thr Ile Leu Val Gly Asp Pro Asn Ser Leu Ser Asn
        995                 1000                1005
Gly Gly Arg Ala Thr Arg Ala Ile Asp Ile Phe Ser Leu Gly Leu Val
    1010                1015                1020
Phe Phe Tyr Val Leu Thr Asn Gly Ser His Pro Phe Asp Cys Gly Asp
1025                1030                1035                1040
Arg Tyr Met Arg Glu Val Asn Ile Arg Lys Gly Asn Tyr Asn Leu Asp
                1045                1050                1055
Pro Leu Asp Ala Leu Gly Asp Phe Ala Tyr Glu Ala Lys Asp Leu Ile
            1060                1065                1070
Ala Ser Met Leu Gln Ala Ser Pro Lys Ala Arg Pro Asp Ser Arg Glu
        1075                1080                1085
Val Met Ala His Pro Phe Phe Trp Ser Pro Lys Lys Arg Leu Ala Phe
    1090                1095                1100
Leu Cys Asp Val Ser Asp Ser Leu Glu Lys Glu Val Arg Asp Pro Pro
1105                1110                1115                1120
Pro Ala Leu Val Glu Leu Glu Arg His Ala Pro Glu Val Ile Lys Gly
                1125                1130                1135
Asp Phe Leu Lys Val Leu Thr Arg Asp Phe Val Glu Ser Leu Gly Lys
            1140                1145                1150
Gln Arg Lys Tyr Thr Gly Asn Lys Leu Leu Asp Leu Leu Arg Ala Leu
        1155                1160                1165
Arg Asn Lys Arg Asn His Tyr Glu Asp Met Ser Asp Ser Leu Lys Arg
    1170                1175                1180
Ser Val Gly Ser Leu Pro Asp Gly Tyr Leu Ala Tyr Trp Thr Val Lys
1185                1190                1195                1200
Phe Pro Met Leu Leu Leu Thr Cys Trp Asn Val Val Tyr Asn Leu Glu
                1205                1210                1215
Trp Glu Lys Thr Asp Arg Phe Arg Glu Tyr Tyr Glu Pro Ala Gly Leu
            1220                1225                1230
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<210> 15
<211> 1669
<212> DNA
<213> Aspergillus niger

<400> 15

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ttatgacacg gtggcctgtg ttcctgtgac acgggcaagc agacgtcctc cacaagctgt     180
gtcgacctac atcaccgtcc tcccttgcag tgcggttaag ataaggctca tagtaaatcg     240
attgatccac aattaaagat caatcacctg tcacgcttga aatgatggaa gaagcattct     300
ctccagtcga ctccctcgcc ggctccccga cgcctgagtt gccattgttg acagtgtccc     360
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agaagcctgt gaagaagaga aagtcatggg gccaggaatt gccagtcccg aagactaact     480
tgcccccaag gaaacgggcc aagactgaag atgagaaaga gcaacgtcgt atcgagcgcg     540
ttcttcgcaa tcgtgcggca gcacaaacat cacgcgagcg caagaggctc gaaatggaga     600
agttggaaaa tgagaagatt cagatggaac agcaaaacca gttccttctg caacgactat     660
cccagatgga agctgagaac aatcgcttaa accaacaagt cgctcaacta tctgctgagg     720
tccggggctc ccgtggcaac actcccaagc ccggctcccc cgtctcagct tctcctaccc     780
taactcctac cctatttaaa caagaacgcg acgaaatccc tcttgaacgg attcctttcc     840
ccacaccctc tatcaccgac tactccccta ccttgaggcc ttccactctg gctgagtcct     900
ccgacgtgac acaacatcct gcagcggtgt tgtgcgacct gcagtgtccg tcgctggact     960
cgaaggagaa ggaagtgccc tctctctctt tgacgtcggc tcaaaccctg aacctcacgc    1020
tgccgatgat cttgcagctc ctctttctga cgatgacttc caccgcctat tcaacgttga    1080
ttcacccgtt gggtcagatt cttcagtcct tgaagacggg ttcgcctttg acgttctcga    1140
cggaggagat ctatcagcat ttccatttga ttctatggtt gatttcgacc ccgaatctgt    1200
tggcttcgaa ggcatcgagc cgccccacgg tcttccggat gagacttctc gccagacttc    1260
tagcgtgcaa cccagccttg gcgcgtccac ttcgcgatgc gacgggcagg gcattgcagc    1320
tggctgttag cgagcagttt cgccagggag atgcatcggc tgtcgatggt aacggagtcc    1380
aatggagctg ggagtctttg ttgaccttgg cgtggacgat agacctactc gaacagccgg    1440
gacgacgcaa acgaatcttg agcggtttga aatcagcgaa aactggacgg cgaagtaata    1500
ttggcaagtc tcaaaggagt acacggagtt catggagttc acgaagcacc caagaggcgt    1560
tgacgtctct ccttatgggc aagcatagtt gaggttccgg ctgtaaatta tcataaatcc    1620
ttataatttt attctagatt tcaatacagc agttgattgt ctgctcatc                1669
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<210> 16
<211> 386
<212> PRT
<213> Aspergillus niger

<400> 16

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Met Val Leu Lys Asp Thr Cys Pro Ser Trp Pro Tyr Pro Ser Cys Cys
 1               5                  10                  15
Leu Val His Leu Thr Pro Gly Thr Thr Trp Pro Gly Leu Ala Pro Pro
            20                  25                  30
Ala Ser Pro Val Met Thr Arg Trp Pro Val Phe Leu Met Met Glu Glu
        35                  40                  45
Ala Phe Ser Pro Val Asp Ser Leu Ala Gly Ser Pro Thr Pro Glu Leu
    50                  55                  60
Pro Leu Leu Thr Val Ser Pro Ala Asp Thr Ser Leu Asp Asp Ser Ser
65                  70                  75                  80
Val Gln Ala Gly Glu Thr Lys Ala Glu Glu Lys Lys Pro Val Lys Lys
                85                  90                  95
Arg Lys Ser Trp Gly Gln Glu Leu Pro Val Pro Lys Thr Asn Leu Pro
            100                 105                 110
Pro Arg Lys Arg Ala Lys Thr Glu Asp Glu Lys Glu Gln Arg Arg Ile
        115                 120                 125
Glu Arg Val Leu Arg Asn Arg Ala Ala Ala Gln Thr Ser Arg Glu Arg
    130                 135                 140
Lys Arg Leu Glu Met Glu Lys Leu Glu Asn Glu Lys Ile Gln Met Glu
145                 150                 155                 160
Gln Gln Asn Gln Phe Leu Leu Gln Arg Leu Ser Gln Met Glu Ala Glu
                165                 170                 175
Asn Asn Arg Leu Asn Gln Gln Val Ala Gln Leu Ser Ala Glu Val Arg
            180                 185                 190
Gly Ser Arg Gly Asn Thr Pro Lys Pro Gly Ser Pro Val Ser Ala Ser
        195                 200                 205
Pro Thr Leu Thr Pro Thr Leu Phe Lys Gln Glu Arg Asp Glu Ile Pro
    210                 215                 220
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```
Leu Glu Arg Ile Pro Phe Pro Thr Pro Ser Ile Thr Asp Tyr Ser Pro
225                 230                 235                 240
Thr Leu Arg Pro Ser Thr Leu Ala Glu Ser Ser Asp Val Thr Gln His
                245                 250                 255
Pro Ala Val Ser Val Ala Gly Leu Glu Gly Glu Gly Ser Ala Leu Ser
            260                 265                 270
Leu Phe Asp Val Gly Ser Asn Pro Glu Pro His Ala Ala Asp Asp Leu
        275                 280                 285
Ala Ala Pro Leu Ser Asp Asp Asp Phe His Arg Leu Phe Asn Val Asp
    290                 295                 300
Ser Pro Val Gly Ser Asp Ser Ser Val Leu Glu Asp Gly Phe Ala Phe
305                 310                 315                 320
Asp Val Leu Asp Gly Gly Asp Leu Ser Ala Phe Pro Phe Asp Ser Met
                325                 330                 335
Val Asp Phe Asp Pro Glu Ser Val Gly Phe Glu Gly Ile Glu Pro Pro
            340                 345                 350
His Gly Leu Pro Asp Glu Thr Ser Arg Gln Thr Ser Ser Val Gln Pro
        355                 360                 365
Ser Leu Gly Ala Ser Thr Ser Arg Cys Asp Gly Gln Gly Ile Ala Ala
    370                 375                 380
Gly Cys
385
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<210> 17
<211> 20
<212> DNA
<213> Aspergillus niger

<400> 17
cggtgttgtg cgacctgcag 20

<210> 18
<211> 44
<212> PRT
<213> Aspergillus niger

<400> 18
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Met Val Leu Lys Asp Thr Cys Pro Ser Trp Pro Tyr Pro Ser Cys Cys
 1               5                  10                  15
Leu Val His Leu Thr Pro Gly Thr Thr Trp Pro Gly Leu Ala Pro Pro
            20                  25                  30
Ala Ser Pro Val Met Thr Arg Trp Pro Val Phe Leu
        35                  40
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<210> 19
<211> 342
<212> PRT
<213> Aspergillus niger

<400> 19
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Met Met Glu Glu Ala Phe Ser Pro Val Asp Ser Leu Ala Gly Ser Pro
 1               5                  10                  15
Thr Pro Glu Leu Pro Leu Leu Thr Val Ser Pro Ala Asp Thr Ser Leu
            20                  25                  30
Asp Asp Ser Ser Val Gln Ala Gly Glu Thr Lys Ala Glu Glu Lys Lys
        35                  40                  45
Pro Val Lys Lys Arg Lys Ser Trp Gly Gln Glu Leu Pro Val Pro Lys
```

```
    50                  55                  60
Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys Thr Glu Asp Glu Lys Glu
65                  70                  75                  80
Gln Arg Arg Ile Glu Arg Val Leu Arg Asn Arg Ala Ala Ala Gln Thr
                85                  90                  95
Ser Arg Glu Arg Lys Arg Leu Glu Met Glu Lys Leu Glu Asn Glu Lys
            100                 105                 110
Ile Gln Met Glu Gln Gln Asn Gln Phe Leu Leu Gln Arg Leu Ser Gln
        115                 120                 125
Met Glu Ala Glu Asn Asn Arg Leu Asn Gln Gln Val Ala Gln Leu Ser
    130                 135                 140
Ala Glu Val Arg Gly Ser Arg Gly Asn Thr Pro Lys Pro Gly Ser Pro
145                 150                 155                 160
Val Ser Ala Ser Pro Thr Leu Thr Pro Thr Leu Phe Lys Gln Glu Arg
                165                 170                 175
Asp Glu Ile Pro Leu Glu Arg Ile Pro Phe Pro Thr Pro Ser Ile Thr
            180                 185                 190
Asp Tyr Ser Pro Thr Leu Arg Pro Ser Thr Leu Ala Glu Ser Ser Asp
        195                 200                 205
Val Thr Gln His Pro Ala Val Ser Val Ala Gly Leu Glu Gly Glu Gly
    210                 215                 220
Ser Ala Leu Ser Leu Phe Asp Val Gly Ser Asn Pro Glu Pro His Ala
225                 230                 235                 240
Ala Asp Asp Leu Ala Ala Pro Leu Ser Asp Asp Asp Phe His Arg Leu
                245                 250                 255
Phe Asn Val Asp Ser Pro Val Gly Ser Asp Ser Ser Val Leu Glu Asp
            260                 265                 270
Gly Phe Ala Phe Asp Val Leu Asp Gly Gly Asp Leu Ser Ala Phe Pro
        275                 280                 285
Phe Asp Ser Met Val Asp Phe Asp Pro Glu Ser Val Gly Phe Glu Gly
    290                 295                 300
Ile Glu Pro Pro His Gly Leu Pro Asp Glu Thr Ser Arg Gln Thr Ser
305                 310                 315                 320
Ser Val Gln Pro Ser Leu Gly Ala Ser Thr Ser Arg Cys Asp Gly Gln
                325                 330                 335
Gly Ile Ala Ala Gly Cys
            340
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<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
atcgcaggat tcccacctac gacaacaacc gccact 36

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
tacagcggat ccctatggat tacgccaatt gtcaag 36

<210> 22
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 22
ccacctacga caacaaccgc cactatggaa atgactgatt ttgaactact tgcctcgtcc 60
ccgccgggtc ac 72

<210> 23
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 23
aattataccc tcttgcgatt gtcttcatga agtgatgaag aaatcattga cactggatgg 60
cggcgttagt atcga 75

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
gccatccttg gtgactgagc c 21

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
caattgctcg ctcttacatt gaat 24

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 26
aattaaccct cactaaaggg 20

<210> 27
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
tggttgatga cgacgatgcg aacagtcatg acaggcaacg 40

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> HAC1-specific oligonucleotide

<400> 28
gggagacgac tgctggaacg ccat 24

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
ccccgagcag tccttgatgg 20

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
gtcgttgatg tcgaagt 17

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
gtaatacgac tcactatagg gc 22

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
ttaggacaga ggccacggtg t 21

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 33
cccatccttg gtgactgagc c 21

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 34
aagagtcggt gtcagagttg g 21

<210> 35
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 35
attaatattt tagcactttg aaaaatgcgt ctacttcgaa gaaacatgct tgcctcgtcc 60
ccgccgggtc ac 72

<210> 36
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 36
aagcagaggg gcatgaacat gttatgaata caaaaattca cgtaaaatgt cgacactgga 60
tggcggcgtt agtat 75

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 37
ccgcaacacg acacggcagg caac 24

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 38
ctaggtagac gttgtatttt g 21

<210> 39
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 39
tcgaacggat ccgaaaagaa gcccgtcaag aagagg 36

<210> 40
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 40
atcgcaggat ccctaggttt ggccatcccg cgagccaaa 39

<210> 41
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 41
cggctgaacc agcgcggcag ccagatgtgg ccaaaggg 38

<210> 42

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 42
ggtacctgct aaccagcgcg gcatgattca ac 32

<210> 43
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 43
ggatcttgca tagccagatg tggcctcgat tgact 35

<210> 44
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 44
ggattagaaa acgccaacgt gtccataacg gtc 33

<210> 45
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 45
gggcgtggag aagcgagaag tggcctcttc ttctcc 36

<210> 46
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> binding consensus sequence

<221> misc_feature
<222> (1)...(11)
<223> n = AW or C

<400> 46
gcsarngtgk c 11

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
gtggtaatat tacctttaca g 21

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
caatttcaat acgggtggac 20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
tgtcatcact gctccatctt 20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 50
ttaagccttg gcaacatatt 20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 51
ttgaacagca gatcgttact g 21

<210> 52

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 52
tataaagttc gtcaatagtg g 21

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 53
cggaggcaag agtcatagac g 21

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 54
caatatattt ctgaaccagt acg 23

<210> 55
<211> 45
<212> RNA
<213> Trichoderma reesei

<400> 55
acugauucga cacaacgucc ugcagagaug uugugcgacc cgcag 45

<210> 56
<211> 45
<212> RNA
<213> Aspergillus nidulans

<400> 56
cccgauuuga cacaacaucc ugcagcgaug uugugcgacc ugcag 45

<210> 57
<211> 28
<212> RNA
<213> Saccharomyces cerevisiae

<400> 57
ccuuguacug uccgaagcgc agucaggu 28

<210> 58

<211> 60
<212> DNA
<213> Trichoderma reesei

<400> 58
ccactgattc gacacaacgt cctgcagaga tgttgtgcga cccgcagtgt caatcggtgg 60

<210> 59
<211> 60
<212> DNA
<213> Aspergillus nidulans

<400> 59
cccccgattt gacacaacat cctgcagcga tgttgtgcga cctgcagtgt cagtcggcgg 60

<210> 60
<211> 68
<212> PRT
<213> Saccharomyces cerevisiae

<400> 60
Lys Ser Thr Leu Pro Pro Arg Lys Arg Ala Lys Thr Lys Glu Glu Lys
 1   5   10   15
Glu Gln Arg Arg Ile Glu Arg Ile Leu Arg Asn Arg Arg Ala Ala His
            20   25   30
Gln Ser Arg Glu Lys Lys Arg Leu His Leu Gln Tyr Leu Glu Arg Lys
        35   40   45
Cys Ser Leu Leu Glu Asn Leu Leu Asn Ser Val Asn Leu Glu Lys Leu
    50   55   60
Ala Asp His Glu
65

<210> 61
<211> 12
<212> DNA
<213> Trichoderma reesei

<400> 61
gccagatgtg gc 12

<210> 62
<211> 11
<212> DNA
<213> Trichoderma reesei

<400> 62
gccaacgtgt c 11

<210> 63
<211> 12
<212> DNA
<213> Trichoderma reesei

<400> 63
gcgagaagtg gc 12